

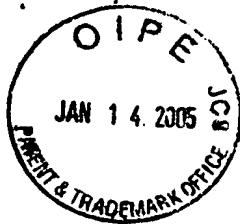


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## FIGURE 6A

SEQ ID NO:8 (nucleic acid sequence)  
SEQ ID NO:7 (amino acid sequence)

|      |   |      |
|------|---|------|
| -792 | CTTAAATACCACAATAGGAAAATTATCAATAAAGCTTTCGGATTCATTACGTTATATC    | -733 |
| -732 | GCAAAAAAAATAGTCGAGCTTCTGAACCGTTCTTAATAAAAAAAATAGTTTTCAGATT    | -673 |
| -672 | TCTATGTGAGGCAGTCAGGATAGAAATTCCATCGAACCTCGTCAGGCCAAATGTGAATGCG | -613 |
| -612 | GCTTTCAAAAGCTTGTCAAATTGGGATGGGAATCCATGAATCGAACATGTCAAAATGG    | -553 |
| -552 | GGGATCACAAAAGTACACTCACGAGGAAAATCAAACCTCTCGTACCTTAAACACATAC    | -493 |
| -492 | GGAAATGATCGATCGATTGAGAAGATTCTCAATGATTTCGTCAATATAAGGTATCTG     | -433 |
| -432 | AGGTATTATGGACCGATTCTGAATAACATCATATACATCGGGCTTGTCCCTGTCCCCAG   | -373 |
| -372 | AGATTCGATGAAAAAAGCGAATTATTCTAATATTGAAGCATGCCAACATGGGCA        | -313 |
| -312 | GTTGATTGTTGTGAGGGTAAAATATCATGAATTGCACCATCAAATGCAGCAAGATATTG   | -253 |
| -252 | ACCAATCCTATAATAGAAAACAGACTTACCAACAAATAGATGIGATGACGATATTATGAA  | -193 |
| -192 | TCTCCAGATGAAAGGCTCGAAAGCTATGAAGCCTCTGAAACCTTTCATGGTGAGATAAT   | -133 |
| -132 | ATTTGCAAATTCCACGAACCTCTAAACGCAATTATGAAATATAAAGGAAAAATAATA     | -73  |
| -72  | TTTCCATATAGCAAGCAAATCAAGCTGCACTCCTCATCCTTAAACTAATAATCTTAC     | -13  |
| -12  | CATTTGATACCAATGGTCAAAGGTAAATGTTATAGGGTTCAAATAGAATCCCAGTCACT   | 48   |
| 1    | MetValLysGlyAsnValIleValValSerAsnArgIleProValThr              | 16   |
| 49   | ATTAAGAAGACTGAGATGATGAAAATGGAAAATCAAGATACTGACTATACAATGTCATCA  | 108  |
| 17   | IleLysLysThrGluAspAspGluAsnGlyLysSerArgTyrAspTyrThrMetSerSer  | 36   |
| 109  | GGCGGATTAGTGACGGCATTACAAGGGCTCAAAATCCATTGATGGTTGGATGGCCT      | 168  |
| 37   | GlyGlyLeuValThrAlaLeuGlnGlyLeuLysAsnProPheArgTrpPheGlyTrpPro  | 56   |
| 169  | GGGATGTCCTGTTGATAGCGAACAGGGACGACAAACTGTCGAGCGGGATTGAAAGGAAAAG | 228  |
| 57   | GlyMetSerValAspSerGluGlnGlyArgGlnThrValGluArgAspLeuLysGluLys  | 76   |
| 229  | TTCAATTGTTATCGATATGGTTAACGTGACGAAATTGCAAGACTTACATTATAACGGCTT  | 288  |
| 77   | PheAsnCysTyrProIleTrpLeuSerAspGluIleAlaAspLeuHisTyrAsnGlyPhe  | 96   |
| 289  | AGCAATTCTATACTTGGCCATTGTTCCACTATCACCCAGGGAGATGAAATTGATGAA     | 348  |
| 97   | SerAsnSerIleLeuTrpProLeuPheHisTyrHisProGlyGluMetAsnPheAspGlu  | 116  |
| 349  | ATTGCTGGGCCCTATTGGAAGCGAAATAAAACTGTTTGCCAAACGATCTTAAAGGAG     | 408  |
| 117  | IleAlaTrpAlaAlaTyrLeuGluAlaAsnLysLeuPheCysGlnThrIleLeuLysGlu  | 136  |
| 409  | ATAAAAGACGGGGACGTTATCTGGGTACATGATTATCATCTCATGTTGCTTCACTG      | 468  |
| 137  | IleLysAspGlyAspValIleTrpValHisAspTyrHisLeuMetLeuLeuProSerLeu  | 156  |
| 469  | CTAAGAGACCAACTTAATAGTAAGGGCTACCGAATGTCAAAATTGGCTTTCCCTTCAT    | 528  |
| 157  | LeuArgAspGlnLeuAsnSerLysGlyLeuProAsnValLysIleGlyPhePheLeuHis  | 176  |
| 529  | ACTCCTTTCCCTCAAGCGAAATATACAGGATACTCCTGTAAGGAAAGAAATTCTCGAA    | 588  |
| 177  | ThrProPheProSerSerGluIleTyrArgIleLeuProValArgLysGluIleLeuGlu  | 196  |
| 589  | GGAGTGCTTAGTTGATAGGTTCCACACCTATGATTATGTCGGTCACTTCT            | 648  |
| 197  | GlyValLeuSerCysAspLeuIleGlyPheHisThrTyrAspTyrValArgHisPheLeu  | 216  |
| 649  | AGTCGGTTGAAAGAATTGAAATTGCGAACGAGCCCACAAGGTGTTGTCTATAATGAT     | 708  |
| 217  | SerSerValGluArgIleLeuLysLeuArgThrSerProGlnGlyValValTyrAsnAsp  | 236  |



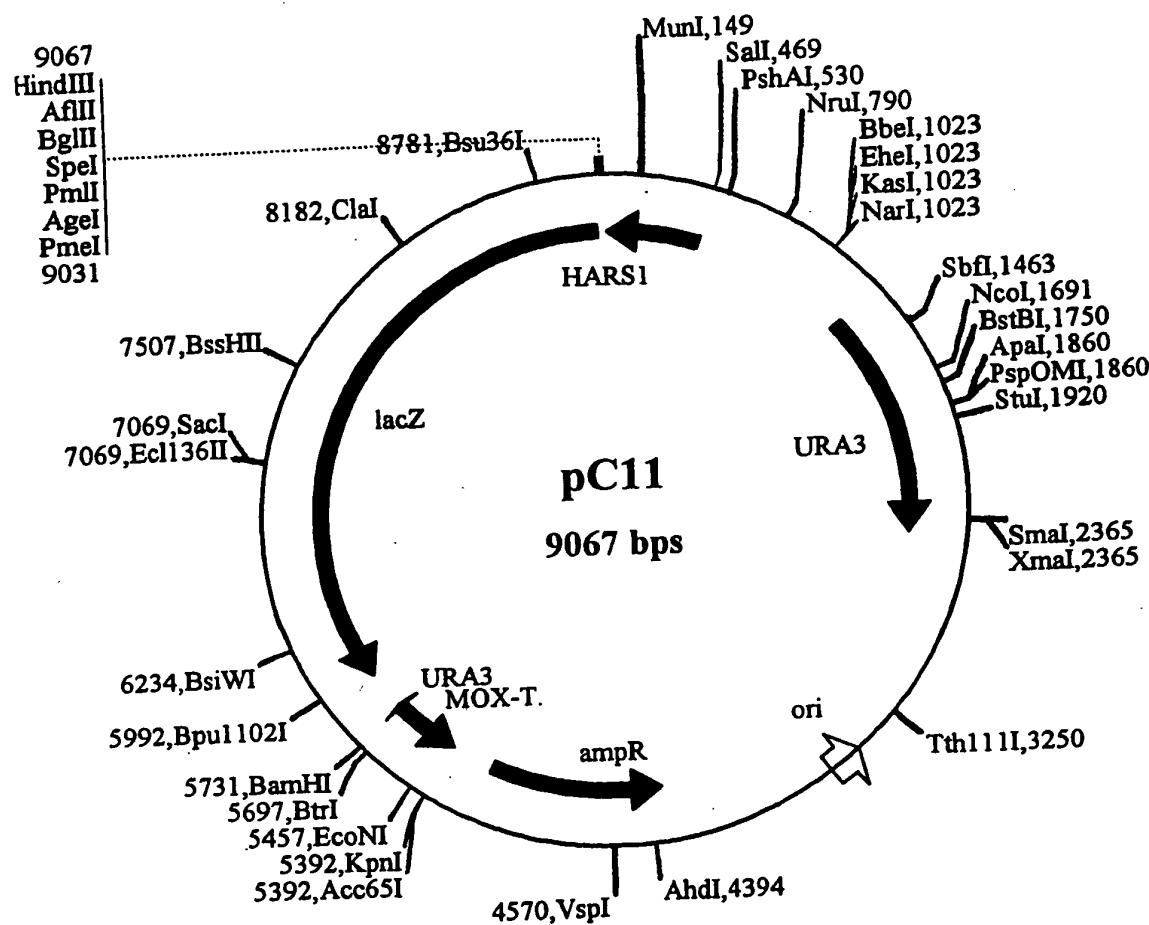
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## FIGURE 6B

|      |   |      |
|------|---|------|
| 709  | AGACAGGTGACTGTAAGTGCTTATCCGATTGGCATTGACGTTGACAAATTCTGAATGGT     | 768  |
| 237  | ArgGlnValThrValSerAlaTyrProIleGlyIleAspValAspLysPheLeuAsnGly    | 256  |
| 769  | CTTAAAGACTGATGAGGTCAAAAGCAGGATAAAACAGCTGGAAACAGATTTGGTAAAGAT    | 828  |
| 257  | LeuLysThrAspGluValLysSerArgIleLysGlnLeuGluThrArgPheGlyLysAsp    | 276  |
| 829  | TGTAAAACCTTATTATTGGGGTGGACAGGGCTGGATTACATCAAAGGTGTACCTCAAAACCTC | 888  |
| 277  | CysLysLeuIleIleGlyValAspArgLeuAspTyrIleLysGlyValProGlnLysLeu    | 296  |
| 889  | CACCGCGTTGAAATTTCCTGGAGAGACACCTCTGAGTGGATTGGAAAAGTTGTTTGATA     | 948  |
| 297  | HisAlaPheGluIlePheLeuGluArgHisProGluTrpIleGlyLysValValLeuIle    | 316  |
| 949  | CAGGTGGCTGTCCCCTCACGAGGGACGTTGAAAGAATATCAATCTTGAGGGCAGCTGTA     | 1008 |
| 317  | GlnValAlaValProSerArgGlyAspValGluGluTyrGlnSerLeuArgAlaAlaVal    | 336  |
| 1009 | AATGAGCTAGTGGGAAGAACATCAATGGTAGATTGGTACCGTCAAGATTGTTCTATCCAT    | 1068 |
| 337  | AsnGluLeuValGlyArgIleAsnGlyArgPheGlyThrValGluPheValProIleHis    | 356  |
| 1069 | TTCCTTCATAAAAGCGTGAACCTCCAAGAGCTGATATCTGTCTACGCTGCTAGTGATGTT    | 1128 |
| 357  | PheLeuHisLysSerValAsnPheGlnGluLeuIleSerValTyrAlaAlaSerAspVal    | 376  |
| 1129 | TGTGTAGTGTACCGACACGGGACCGGAATGAATTGGTCAGTTATGAATAACATTGCTTGT    | 1188 |
| 377  | CysValValSerSerThrArgAspGlyMetAsnLeuValSerTyrGluTyrIleAlaCys    | 396  |
| 1189 | CAACAAGATCGAAAGGGATCTCTAGTACTAAGTGAATTGCGGGAGCTGCTCAGTCATTA     | 1248 |
| 397  | GlnGlnAspArgLysGlySerLeuValLeuSerGluPheAlaGlyAlaAlaGlnSerLeu    | 416  |
| 1249 | AATGGCGCTCTGGTAGTGAATCCATGGAATACAGAACACTCAGTGAAGCTATTTACGAA     | 1308 |
| 417  | AsnGlyAlaLeuValValAsnProTrpAsnThrGluGluLeuSerGluAlaIleTyrGlu    | 436  |
| 1309 | GGCTTGATCATGAGTGAAGAGAAAAGGAGGGCAATTTCAGAAGATGTTCAAGTACATT      | 1368 |
| 437  | GlyLeuIleMetSerGluGluLysArgArgGlyAsnPheGlnLysMetPheLysTyrIle    | 456  |
| 1369 | GAGAAATATACTGCAAGTTATTGGGGAGAGAACCTTGAAAGAATTGACGAGAGTGTGA      | 1428 |
| 457  | GluLysTyrThrAlaSerTyrTrpGlyGluAsnPheValLysGluLeuThrArgVal       | 476  |
| 1429 | TTACTGGTTGCAGGTAAATTGAAATGTTCACTTGTACTTGAAGAACATTATATTAT        | 1488 |
| 1489 | ATACATGTTATACATCAATAGGATAAAAATTAAAGTAGACAAAGTTATCATTGGGGC       | 1548 |
| 1549 | TGAAAAAAATGAAACGATAACAATATAATTGACAAAATTAAATTGATCTAATTGAGCTGGA   | 1608 |
| 1609 | GGGCGTAATATATTGGGTTCCCTGAATCATCTTGTAGATCACAATATGGGGCAGCTCTT     | 1668 |
| 1669 | TCGCAGCCGATCACAGAGAACACATCACACTGTCCAACATGATCACATATGCAATTCA      | 1728 |
| 1729 | ATCGGGAAAATGCAAGGATACAGGTTGACCATGGAAGACGCGGTTCTGIGATTGAAACGAA   | 1788 |
| 1789 | AGAATAATCGTGACGGAAGAGGGACTTGACATCAGAAAACAAGACGAGAATACAGAGGGT    | 1848 |
| 1849 | GATCTGGAGTCTCTCAAATTAAACATTATGGTGTCTTGACGGACATGGCGGT            | 1903 |



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**FIGURE 7**



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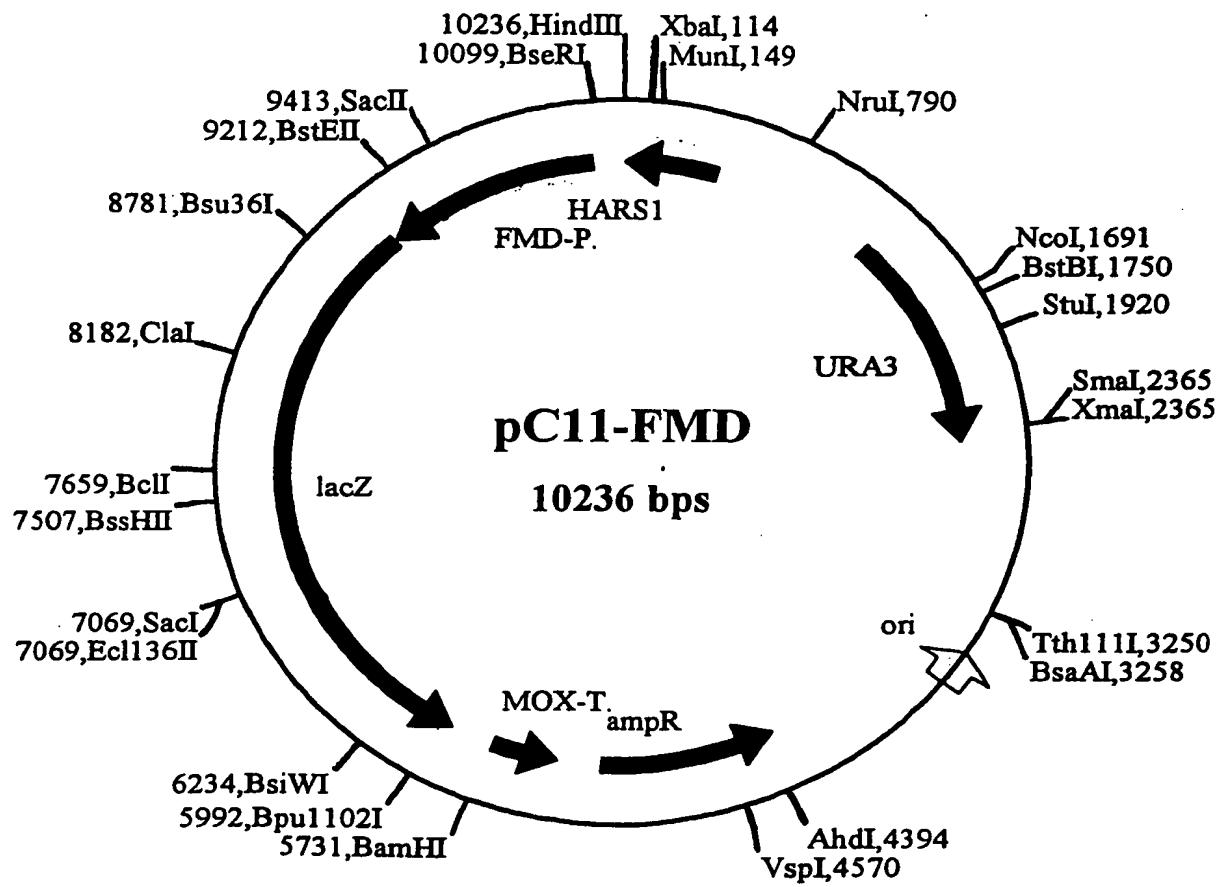
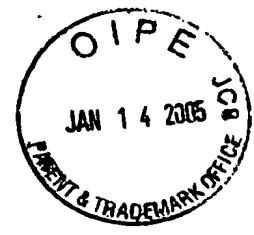
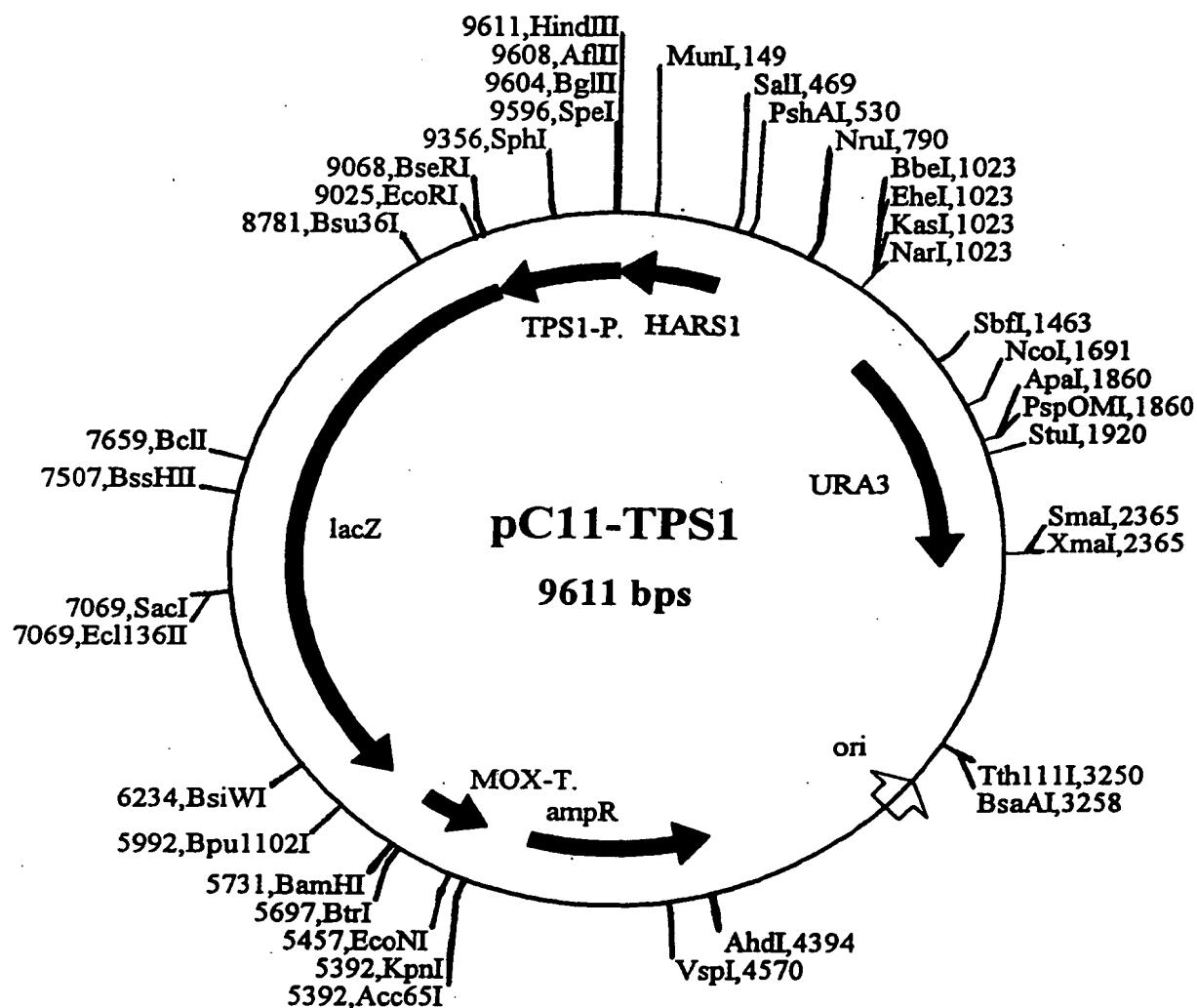


FIGURE 8



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**FIGURE 9**



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FIG. 10A

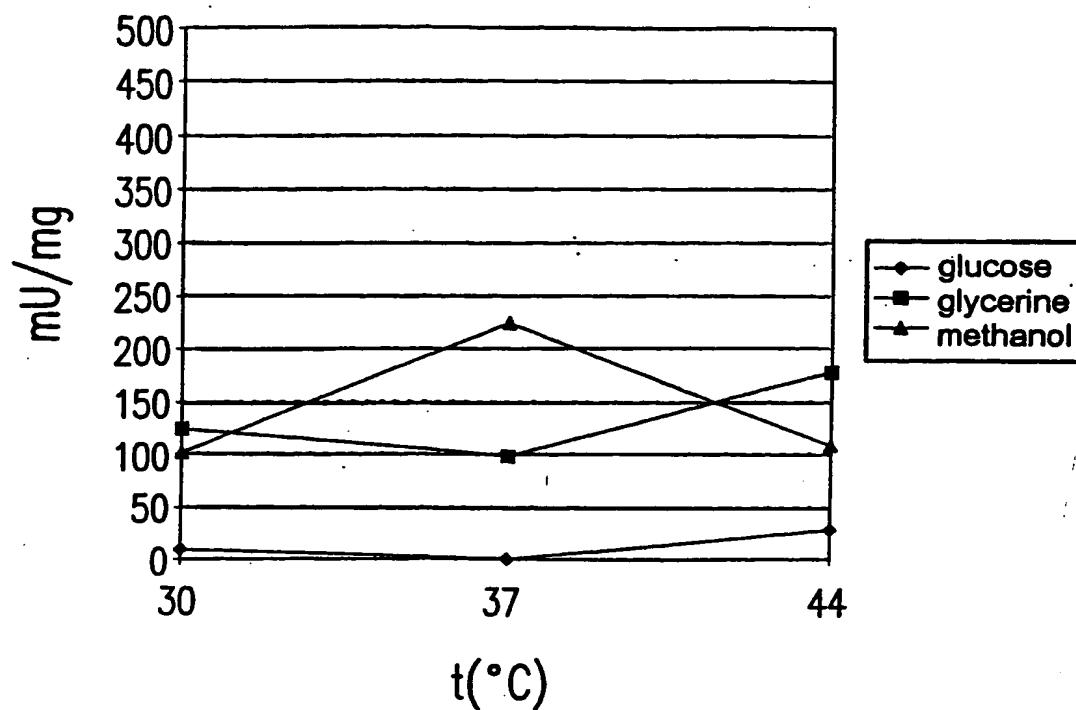
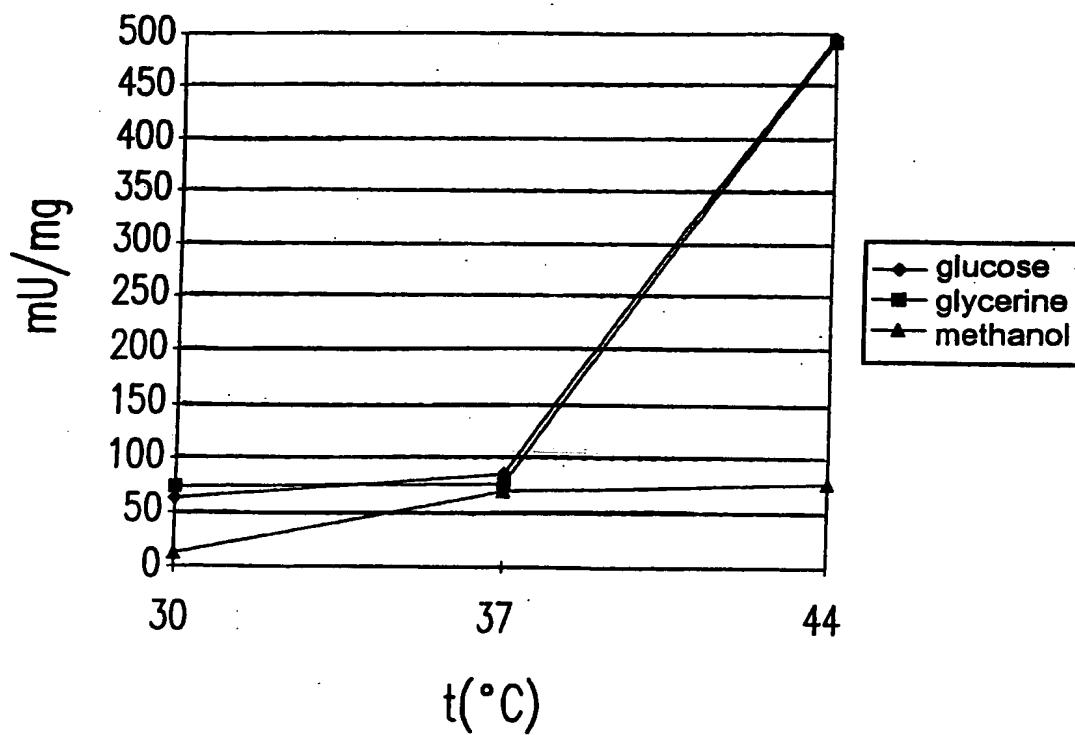


FIG. 10B





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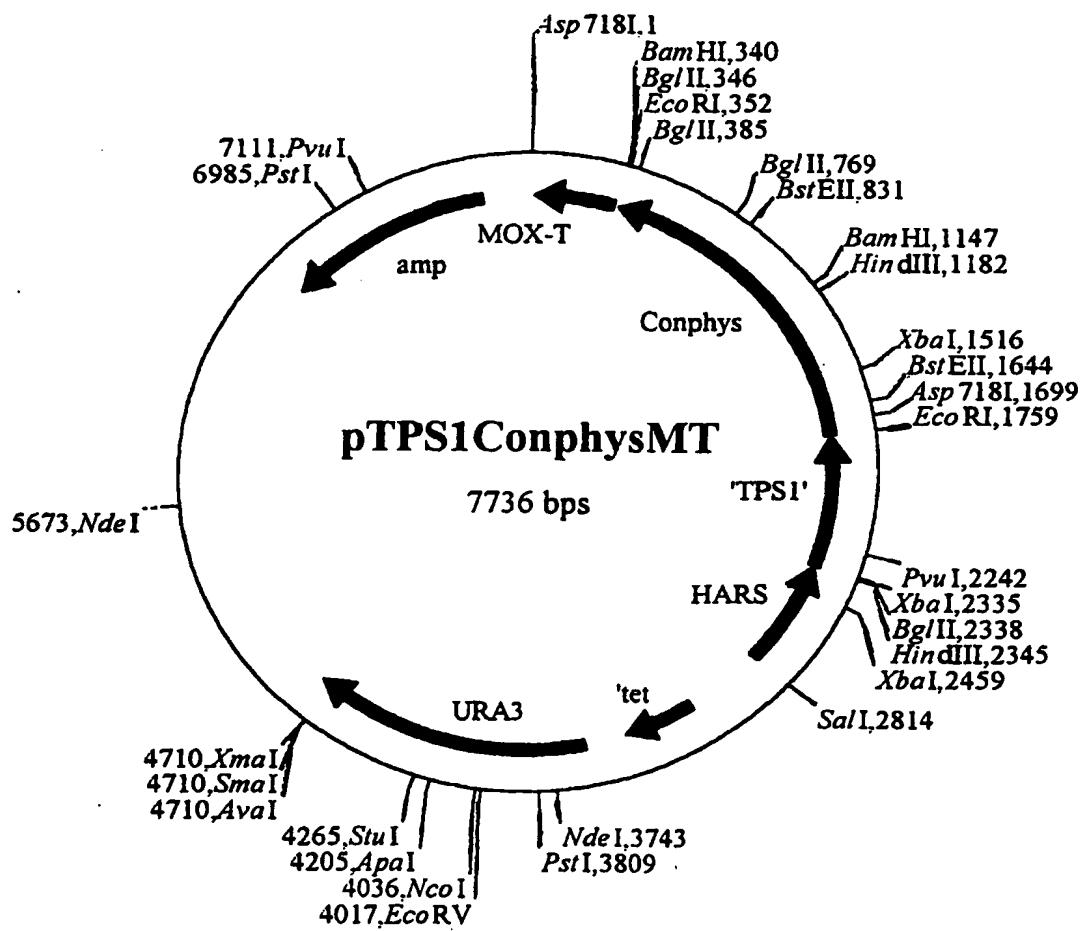


FIG. 11